RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/712,795A_
Source: _1Fw/6_
Date Processed by STIC: _7/19/06_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 07/19/2006
PATENT APPLICATION: US/10/712,795A   TIME: 09:01:20

Input Set : A:\DOC0216USSEQ2.txt
Output Set: N:\CRF4\07192006\J712795A.raw

```
 3 <110> APPLICANT: Rosanne M. Crooke
 4        Mark J. Graham
 5        Kristina Lemonidis Tarbet
 6        Kenneth W. Dobie
 7        Susan M. Freier
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
12 <130> FILE REFERENCE: DOC-0216US(ISIS.003CP1)
14 <140> CURRENT APPLICATION NUMBER: US 10/712,795A
15 <141> CURRENT FILING DATE: 2003-11-13
17 <150> PRIOR APPLICATION NUMBER: US 60/426,234
18 <151> PRIOR FILING DATE: 2002-11-13
20 <150> PRIOR APPLICATION NUMBER: PCT/US03/15493
21 <151> PRIOR FILING DATE: 2003-05-15
23 <160> NUMBER OF SEQ ID NOS: 897
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 20
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Antisense Oligonucleotide
33 <400> SEQUENCE: 1
34 tccgtcatcg ctcctcaggg                                            20
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 20
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Antisense Oligonucleotide
44 <400> SEQUENCE: 2
45 atgcattctg cccccaagga                                            20
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 14121
49 <212> TYPE: DNA
50 <213> ORGANISM: Homo sapiens
52 <220> FEATURE:
53 <221> NAME/KEY: CDS
54 <222> LOCATION: (129)..(13820)
56 <400> SEQUENCE: 3
57 attcccaccg ggacctgcgg ggctgagtgc ccttctcggt tgctgccgct gaggagcccg 60
59 cccagccagc cagggccgcg aggccgaggc caggccgcag cccaggagcc gccccaccgc 120
61 agctggcg atg gac ccg ccg agg ccc gcg ctg ctg gcg ctg ctg gcg ctg 170
62           Met Asp Pro Pro Arg Pro Ala Leu Leu Ala Leu Leu Ala Leu
63             1               5                  10
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65 cct gcg ctg ctg ctg ctg ctg ctg gcg ggc gcc agg gcc gaa gag gaa    218
66 Pro Ala Leu Leu Leu Leu Leu Leu Ala Gly Ala Arg Ala Glu Glu Glu
67  15                  20                  25                  30
69 atg ctg gaa aat gtc agc ctg gtc tgt cca aaa gat gcg acc cga ttc    266
70 Met Leu Glu Asn Val Ser Leu Val Cys Pro Lys Asp Ala Thr Arg Phe
71                      35                  40                  45
74 aag cac ctc cgg aag tac aca tac aac tat gag gct gag agt tcc agt    314
75 Lys His Leu Arg Lys Tyr Thr Tyr Asn Tyr Glu Ala Glu Ser Ser Ser
76                  50                  55                  60
78 gga gtc cct ggg act gct gat tca aga agt gcc acc agg atc aac tgc    362
79 Gly Val Pro Gly Thr Ala Asp Ser Arg Ser Ala Thr Arg Ile Asn Cys
80              65                  70                  75
82 aag gtt gag ctg gag gtt ccc cag ctc tgc agc ttc atc ctg aag acc    410
83 Lys Val Glu Leu Glu Val Pro Gln Leu Cys Ser Phe Ile Leu Lys Thr
84      80                  85                  90
86 agc cag tgc acc ctg aaa gag gtg tat ggc ttc aac cct gag ggc aaa    458
87 Ser Gln Cys Thr Leu Lys Glu Val Tyr Gly Phe Asn Pro Glu Gly Lys
88  95                 100                 105                 110
90 gcc ttg ctg aag aaa acc aag aac tct gag gag ttt gct gca gcc atg    506
91 Ala Leu Leu Lys Lys Thr Lys Asn Ser Glu Glu Phe Ala Ala Ala Met
92                 115                 120                 125
94 tcc agg tat gag ctc aag ctg gcc att cca gaa ggg aag cag gtt ttc    554
95 Ser Arg Tyr Glu Leu Lys Leu Ala Ile Pro Glu Gly Lys Gln Val Phe
96                 130                 135                 140
98 ctt tac ccg gag aaa gat gaa cct act tac atc ctg aac atc aag agg    602
99 Leu Tyr Pro Glu Lys Asp Glu Pro Thr Tyr Ile Leu Asn Ile Lys Arg
100                145                 150                 155
102 ggc atc att tct gcc ctc ctg gtt ccc cca gag aca gaa gaa gcc aag    650
103 Gly Ile Ile Ser Ala Leu Leu Val Pro Pro Glu Thr Glu Glu Ala Lys
104     160                 165                 170
106 caa gtg ttg ttt ctg gat acc gtg tat gga aac tgc tcc act cac ttt    698
107 Gln Val Leu Phe Leu Asp Thr Val Tyr Gly Asn Cys Ser Thr His Phe
108 175                 180                 185                 190
110 acc gtc aag acg agg aag ggc aat gtg gca aca gaa ata tcc act gaa    746
111 Thr Val Lys Thr Arg Lys Gly Asn Val Ala Thr Glu Ile Ser Thr Glu
112                 195                 200                 205
114 aga gac ctg ggg cag tgt gat cgc ttc aag ccc atc cgc aca ggc atc    794
115 Arg Asp Leu Gly Gln Cys Asp Arg Phe Lys Pro Ile Arg Thr Gly Ile
116                 210                 215                 220
118 agc cca ctt gct ctc atc aaa ggc atg acc cgc ccc ttg tca act ctg    842
119 Ser Pro Leu Ala Leu Ile Lys Gly Met Thr Arg Pro Leu Ser Thr Leu
120                 225                 230                 235
122 atc agc agc agc cag tcc tgt cag tac aca ctg gac gct aag agg aag    890
123 Ile Ser Ser Ser Gln Ser Cys Gln Tyr Thr Leu Asp Ala Lys Arg Lys
124     240                 245                 250
126 cat gtg gca gaa gcc atc tgc aag gag caa cac ctc ttc ctg cct ttc    938
127 His Val Ala Glu Ala Ile Cys Lys Glu Gln His Leu Phe Leu Pro Phe
128 255                 260                 265                 270
130 tcc tac aac aat aag tat ggg atg gta gca caa gtg aca cag act ttg    986
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131 Ser Tyr Asn Asn Lys Tyr Gly Met Val Ala Gln Val Thr Gln Thr Leu
132             275                 280                 285
134 aaa ctt gaa gac aca cca aag atc aac agc cgc ttc ttt ggt gaa ggt   1034
135 Lys Leu Glu Asp Thr Pro Lys Ile Asn Ser Arg Phe Phe Gly Glu Gly
136             290                 295                 300
138 act aag aag atg ggc ctc gca ttt gag agc acc aaa tcc aca tca cct   1082
139 Thr Lys Lys Met Gly Leu Ala Phe Glu Ser Thr Lys Ser Thr Ser Pro
140             305                 310                 315
142 cca aag cag gcc gaa gct gtt ttg aag act ctc cag gaa ctg aaa aaa   1130
143 Pro Lys Gln Ala Glu Ala Val Leu Lys Thr Leu Gln Glu Leu Lys Lys
144         320                 325                 330
146 cta acc atc tct gag caa aat atc cag aga gct aat ctc ttc aat aag   1178
147 Leu Thr Ile Ser Glu Gln Asn Ile Gln Arg Ala Asn Leu Phe Asn Lys
148 335                 340                 345                 350
150 ctg gtt act gag ctg aga ggc ctc agt gat gaa gca gtc aca tct ctc   1226
151 Leu Val Thr Glu Leu Arg Gly Leu Ser Asp Glu Ala Val Thr Ser Leu
152             355                 360                 365
154 ttg cca cag ctg att gag gtg tcc agc ccc atc act tta caa gcc ttg   1274
155 Leu Pro Gln Leu Ile Glu Val Ser Ser Pro Ile Thr Leu Gln Ala Leu
156             370                 375                 380
158 gtt cag tgt gga cag cct cag tgc tcc act cac atc ctc cag tgg ctg   1322
159 Val Gln Cys Gly Gln Pro Gln Cys Ser Thr His Ile Leu Gln Trp Leu
160         385                 390                 395
162 aaa cgt gtg cat gcc aac ccc ctt ctg ata gat gtg gtc acc tac ctg   1370
163 Lys Arg Val His Ala Asn Pro Leu Leu Ile Asp Val Val Thr Tyr Leu
164         400                 405                 410
166 gtg gcc ctg atc ccc gag ccc tca gca cag cag ctg cga gag atc ttc   1418
167 Val Ala Leu Ile Pro Glu Pro Ser Ala Gln Gln Leu Arg Glu Ile Phe
168 415                 420                 425                 430
170 aac atg gcg agg gat cag cgc agc cga gcc acc ttg tat gcg ctg agc   1466
171 Asn Met Ala Arg Asp Gln Arg Ser Arg Ala Thr Leu Tyr Ala Leu Ser
172             435                 440                 445
174 cac gcg gtc aac aac tat cat aag aca aac cct aca ggg acc cag gag   1514
175 His Ala Val Asn Asn Tyr His Lys Thr Asn Pro Thr Gly Thr Gln Glu
176             450                 455                 460
178 ctg ctg gac att gct aat tac ctg atg gaa cag att caa gat gac tgc   1562
179 Leu Leu Asp Ile Ala Asn Tyr Leu Met Glu Gln Ile Gln Asp Asp Cys
180             465                 470                 475
182 act ggg gat gaa gat tac acc tat ttg att ctg cgg gtc att gga aat   1610
183 Thr Gly Asp Glu Asp Tyr Thr Tyr Leu Ile Leu Arg Val Ile Gly Asn
184         480                 485                 490
186 atg ggc caa acc atg gag cag tta act cca gaa ctc aag tct tca atc   1658
187 Met Gly Gln Thr Met Glu Gln Leu Thr Pro Glu Leu Lys Ser Ser Ile
188 495                 500                 505                 510
190 ctc aaa tgt gtc caa agt aca aag cca tca ctg atg atc cag aaa gct   1706
191 Leu Lys Cys Val Gln Ser Thr Lys Pro Ser Leu Met Ile Gln Lys Ala
192             515                 520                 525
194 gcc atc cag gct ctg cgg aaa atg gag cct aaa gac aag gac cag gag   1754
195 Ala Ile Gln Ala Leu Arg Lys Met Glu Pro Lys Asp Lys Asp Gln Glu
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196            530                535                540
198 gtt ctt ctt cag act ttc ctt gat gat gct tct ccg gga gat aag cga   1802
199 Val Leu Leu Gln Thr Phe Leu Asp Asp Ala Ser Pro Gly Asp Lys Arg
200            545                550                555
202 ctg gct gcc tat ctt atg ttg atg agg agt cct tca cag gca gat att   1850
203 Leu Ala Ala Tyr Leu Met Leu Met Arg Ser Pro Ser Gln Ala Asp Ile
204            560                565                570
206 aac aaa att gtc caa att cta cca tgg gaa cag aat gag caa gtg aag   1898
207 Asn Lys Ile Val Gln Ile Leu Pro Trp Glu Gln Asn Glu Gln Val Lys
208 575                580                585                590
210 aac ttt gtg gct tcc cat att gcc aat atc ttg aac tca gaa gaa ttg   1946
211 Asn Phe Val Ala Ser His Ile Ala Asn Ile Leu Asn Ser Glu Glu Leu
212            595                600                605
214 gat atc caa gat ctg aaa aag tta gtg aaa gaa gct ctg aaa gaa tct   1994
215 Asp Ile Gln Asp Leu Lys Lys Leu Val Lys Glu Ala Leu Lys Glu Ser
216            610                615                620
218 caa ctt cca act gtc atg gac ttc aga aaa ttc tct cgg aac tat caa   2042
219 Gln Leu Pro Thr Val Met Asp Phe Arg Lys Phe Ser Arg Asn Tyr Gln
220            625                630                635
222 ctc tac aaa tct gtt tct ctt cca tca ctt gac cca gcc tca gcc aaa   2090
223 Leu Tyr Lys Ser Val Ser Leu Pro Ser Leu Asp Pro Ala Ser Ala Lys
224            640                645                650
226 ata gaa ggg aat ctt ata ttt gat cca aat aac tac ctt cct aaa gaa   2138
227 Ile Glu Gly Asn Leu Ile Phe Asp Pro Asn Asn Tyr Leu Pro Lys Glu
228 655                660                665                670
231 agc atg ctg aaa act acc ctc act gcc ttt gga ttt gct tca gct gac   2186
232 Ser Met Leu Lys Thr Thr Leu Thr Ala Phe Gly Phe Ala Ser Ala Asp
233            675                680                685
235 ctc atc gag att ggc ttg gaa gga aaa ggc ttt gag cca aca ttg gaa   2234
236 Leu Ile Glu Ile Gly Leu Glu Gly Lys Gly Phe Glu Pro Thr Leu Glu
237            690                695                700
239 gct ctt ttt ggg aag caa gga ttt ttc cca gac agt gtc aac aaa gct   2282
240 Ala Leu Phe Gly Lys Gln Gly Phe Phe Pro Asp Ser Val Asn Lys Ala
241            705                710                715
243 ttg tac tgg gtt aat ggt caa gtt cct gat ggt gtc tct aag gtc tta   2330
244 Leu Tyr Trp Val Asn Gly Gln Val Pro Asp Gly Val Ser Lys Val Leu
245            720                725                730
247 gtg gac cac ttt ggc tat acc aaa gat gat aaa cat gag cag gat atg   2378
248 Val Asp His Phe Gly Tyr Thr Lys Asp Asp Lys His Glu Gln Asp Met
249 735                740                745                750
251 gta aat gga ata atg ctc agt gtt gag aag ctg att aaa gat ttg aaa   2426
252 Val Asn Gly Ile Met Leu Ser Val Glu Lys Leu Ile Lys Asp Leu Lys
253            755                760                765
255 tcc aaa gaa gtc ccg gaa gcc aga gcc tac ctc cgc atc ttg gga gag   2474
256 Ser Lys Glu Val Pro Glu Ala Arg Ala Tyr Leu Arg Ile Leu Gly Glu
257            770                775                780
259 gag ctt ggt ttt gcc agt ctc cat gac ctc cag ctc ctg gga aag ctg   2522
260 Glu Leu Gly Phe Ala Ser Leu His Asp Leu Gln Leu Leu Gly Lys Leu
261            785                790                795
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263 ctt ctg atg ggt gcc cgc act ctg cag ggg atc ccc cag atg att gga   2570
264 Leu Leu Met Gly Ala Arg Thr Leu Gln Gly Ile Pro Gln Met Ile Gly
265     800                 805                 810
267 gag gtc atc agg aag ggc tca aag aat gac ttt ttt ctt cac tac atc   2618
268 Glu Val Ile Arg Lys Gly Ser Lys Asn Asp Phe Phe Leu His Tyr Ile
269 815                 820                 825                 830
271 ttc atg gag aat gcc ttt gaa ctc ccc act gga gct gga tta cag ttg   2666
272 Phe Met Glu Asn Ala Phe Glu Leu Pro Thr Gly Ala Gly Leu Gln Leu
273                 835                 840                 845
275 caa ata tct tca tct gga gtc att gct ccc gga gcc aag gct gga gta   2714
276 Gln Ile Ser Ser Ser Gly Val Ile Ala Pro Gly Ala Lys Ala Gly Val
277                 850                 855                 860
279 aaa ctg gaa gta gcc aac atg cag gct gaa ctg gtg gca aaa ccc tcc   2762
280 Lys Leu Glu Val Ala Asn Met Gln Ala Glu Leu Val Ala Lys Pro Ser
281         865                 870                 875
283 gtg tct gtg gag ttt gtg aca aat atg ggc atc atc att ccg gac ttc   2810
284 Val Ser Val Glu Phe Val Thr Asn Met Gly Ile Ile Ile Pro Asp Phe
285         880                 885                 890
287 gct agg agt ggg gtc cag atg aac acc aac ttc ttc cac gag tcg ggt   2858
288 Ala Arg Ser Gly Val Gln Met Asn Thr Asn Phe Phe His Glu Ser Gly
289 895                 900                 905                 910
291 ctg gag gct cat gtt gcc cta aaa gct ggg aag ctg aag ttt atc att   2906
292 Leu Glu Ala His Val Ala Leu Lys Ala Gly Lys Leu Lys Phe Ile Ile
293                 915                 920                 925
295 cct tcc cca aag aga cca gtc aag ctg ctc agt gga ggc aac aca tta   2954
296 Pro Ser Pro Lys Arg Pro Val Lys Leu Leu Ser Gly Gly Asn Thr Leu
297                 930                 935                 940
299 cat ttg gtc tct acc acc aaa acg gag gtg atc cca cct ctc att gag   3002
300 His Leu Val Ser Thr Thr Lys Thr Glu Val Ile Pro Pro Leu Ile Glu
301         945                 950                 955
303 aac agg cag tcc tgg tca gtt tgc aag caa gtc ttt cct ggc ctg aat   3050
304 Asn Arg Gln Ser Trp Ser Val Cys Lys Gln Val Phe Pro Gly Leu Asn
305         960                 965                 970
307 tac tgc acc tca ggc gct tac tcc aac gcc agc tcc aca gac tcc gcc   3098
308 Tyr Cys Thr Ser Gly Ala Tyr Ser Asn Ala Ser Ser Thr Asp Ser Ala
309 975                 980                 985                 990
311 tcc tac tat ccg ctg acc ggg gac acc aga tta gag ctg gaa ctg agg   3146
312 Ser Tyr Tyr Pro Leu Thr Gly Asp Thr Arg Leu Glu Leu Glu Leu Arg
313                 995                 1000                1005
315 cct aca gga gag att gag cag tat tct gtc agc gca acc tat gag ctc   3194
316 Pro Thr Gly Glu Ile Glu Gln Tyr Ser Val Ser Ala Thr Tyr Glu Leu
317                 1010                1015                1020
319 cag aga gag gac aga gcc ttg gtg gat acc ctg aag ttt gta act caa   3242
320 Gln Arg Glu Asp Arg Ala Leu Val Asp Thr Leu Lys Phe Val Thr Gln
321         1025                1030                1035
323 gca gaa ggt gcg aag cag act gag gct acc atg aca ttc aaa tat aat   3290
324 Ala Glu Gly Ala Lys Gln Thr Glu Ala Thr Met Thr Phe Lys Tyr Asn
325         1040                1045                1050
327 cgg cag agt atg acc ttg tcc agt gaa gtc caa att ccg gat ttt gat   3338
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/19/2006
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:503; N Pos. 44,99,156,468
Seq#:810; N Pos. 45,118,148,173,180
Seq#:855; N Pos. 7,469,470,471,472,473,474,476,477,478,479
Seq#:890; N Pos. 9

VERIFICATION SUMMARY   DATE: 07/19/2006
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L:9405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:503 after pos.:0
M:341 Repeated in SeqNo=503
L:11951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:810 after pos.:0
M:341 Repeated in SeqNo=810
L:12513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:855 after pos.:0
M:341 Repeated in SeqNo=855
L:13143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:890 after pos.:0